

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/976,935A

Source: IFW/6

Date Processed by STIC: 3-30-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/09/976,935A

TIME: 15:14:26

Input Set : A:\36470Asubseq.txt

Output Set: N:\CRF4\03302005\I976935A.raw

5 <110> APPLICANT: Staunton, Donald E.

9 <120> TITLE OF INVENTION: MATERIALS AND METHODS TO MODULATE LIGAND BINDING/ENZYMATIC  
ACTIVITY

10 OF ALPHA/BETA PROTEINS CONTAINING AN ALLOSTERIC REGULATORY SITE

14 <130> FILE REFERENCE: 27866/36470A

18 <140> CURRENT APPLICATION NUMBER: 09/976,935A

20 <141> CURRENT FILING DATE: 2001-10-12

24 <150> PRIOR APPLICATION NUMBER: US 60/239,750

26 <151> PRIOR FILING DATE: 2000-10-12

30 <160> NUMBER OF SEQ ID NOS: 36

34 <170> SOFTWARE: PatentIn version 3.1

38 <210> SEQ ID NO: 1

40 <211> LENGTH: 34

42 <212> TYPE: DNA

44 <213> ORGANISM: D156A

48 <400> SEQUENCE: 1

49 cattgccttc ttgattgcgg gctctggtag catc 34

52 <210> SEQ ID NO: 2

54 <211> LENGTH: 34

56 <212> TYPE: DNA

58 <213> ORGANISM: V254A

62 <400> SEQUENCE: 2

63 gcctttaaga tcctagcggg catcacggat ggag 34

66 <210> SEQ ID NO: 3

68 <211> LENGTH: 34

70 <212> TYPE: DNA

72 <213> ORGANISM: Q327A

76 <400> SEQUENCE: 3

77 gaagaccatt cagaacgcgc ttcgggagaa gatc 34

80 <210> SEQ ID NO: 4

82 <211> LENGTH: 32

84 <212> TYPE: DNA

86 <213> ORGANISM: I332A

90 <400> SEQUENCE: 4

91 cagcttcggg agaaggcgtt tgcgatcgag gg 32

94 <210> SEQ ID NO: 5

96 <211> LENGTH: 32

98 <212> TYPE: DNA

100 <213> ORGANISM: F333A

104 <400> SEQUENCE: 5

105 cttcgggaga agatcgcggc gatcgagggt ac 32

108 <210> SEQ ID NO: 6

110 <211> LENGTH: 33

112 <212> TYPE: DNA

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114 <213> ORGANISM: E336A
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119 gaagatcttt gcgatcgcggtactcagac agg 33
122 <210> SEQ ID NO: 7
124 <211> LENGTH: 30
126 <212> TYPE: DNA
128 <213> ORGANISM: Primer
132 <400> SEQUENCE: 7
133 attggatccg ctggcaccga gattgccatc 30
136 <210> SEQ ID NO: 8
138 <211> LENGTH: 30
140 <212> TYPE: DNA
142 <213> ORGANISM: Primer
146 <400> SEQUENCE: 8
147 aattttctcga ggtctccaac cgtgccttcc 30
150 <210> SEQ ID NO: 9
152 <211> LENGTH: 27
154 <212> TYPE: PRT
156 <213> ORGANISM: Amino acid insertion
160 <400> SEQUENCE: 9
162 Pro Lys Gly Arg His Arg Gly Val Thr Val Val Arg Ser His His Gly
163 1 5 10 15
166 Val Leu Ile Cys Ile Gln Val Leu Val Arg Arg
167 20 25
170 <210> SEQ ID NO: 10
172 <211> LENGTH: 20
174 <212> TYPE: DNA
176 <213> ORGANISM: primer Eo26-H3
180 <400> SEQUENCE: 10
181 gaggggaagc ttagtgggcc 20
184 <210> SEQ ID NO: 11
186 <211> LENGTH: 19
188 <212> TYPE: DNA
190 <213> ORGANISM: primer Eo-24
194 <400> SEQUENCE: 11
195 gaagttggcc tgagcctgg 19
198 <210> SEQ ID NO: 12
200 <211> LENGTH: 25
202 <212> TYPE: DNA
204 <213> ORGANISM: E-cad 5'#1
208 <400> SEQUENCE: 12
209 ctgcctcgct cgggctcccc ggcca 25
212 <210> SEQ ID NO: 13
214 <211> LENGTH: 27
216 <212> TYPE: DNA
218 <213> ORGANISM: E-cad 3'#1
222 <400> SEQUENCE: 13
223 ctgcacatgg tctgggccgc ctctctc 27
226 <210> SEQ ID NO: 14

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228 <211> LENGTH: 45
230 <212> TYPE: DNA
232 <213> ORGANISM: primer Ecad5'Kozak
236 <400> SEQUENCE: 14
237 gcgttaaagc ttcacagctc atcaccatgg gcccttggag ccgca 45
240 <210> SEQ ID NO: 15
242 <211> LENGTH: 33
244 <212> TYPE: DNA
246 <213> ORGANISM: Primer Ecad3'(Xho)
250 <400> SEQUENCE: 15
251 aggcgctcga gaatccccag aatggcagga att 33
254 <210> SEQ ID NO: 16
256 <211> LENGTH: 26
258 <212> TYPE: DNA
260 <213> ORGANISM: primer MAdCAM-1 5'#1
264 <400> SEQUENCE: 16
265 atggatttcg gactggccct cctgct 26
268 <210> SEQ ID NO: 17
270 <211> LENGTH: 24
272 <212> TYPE: DNA
274 <213> ORGANISM: primer MAdCAM-1 3'#5
278 <400> SEQUENCE: 17
279 ctccaagcca ggcagcctca tcgt 24
282 <210> SEQ ID NO: 18
284 <211> LENGTH: 49
286 <212> TYPE: DNA
288 <213> ORGANISM: primer Mad5'Kozak
292 <400> SEQUENCE: 18
293 gcgttaaagc ttcacagctc atcaccatgg atttcggact ggccctcct 49
296 <210> SEQ ID NO: 19
298 <211> LENGTH: 57
300 <212> TYPE: DNA
302 <213> ORGANISM: Primer Mad 3' #6 Sal
306 <400> SEQUENCE: 19
307 gctagtcgac ggggatggcc tggcgggtggc tgagctccaa gcaggcagcc tcatcgt 57
310 <210> SEQ ID NO: 20
312 <211> LENGTH: 28
314 <212> TYPE: DNA
316 <213> ORGANISM: Primer Alpha1.5
320 <400> SEQUENCE: 20
321 gactttcagc ggcccgggtgg aagacatg 28
324 <210> SEQ ID NO: 21
326 <211> LENGTH: 28
328 <212> TYPE: DNA
330 <213> ORGANISM: Primer Alpha1.3
334 <400> SEQUENCE: 21
335 ccagttgagt gctgcattct tgtacagg 28
338 <210> SEQ ID NO: 22
340 <211> LENGTH: 29

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Input Set : A:\36470Asubseq.txt

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342 <212> TYPE: DNA
344 <213> ORGANISM: A1.5Nde
348 <400> SEQUENCE: 22
349 atatcatatg gacatagtca tagtgctgg 29
352 <210> SEQ ID NO: 23
354 <211> LENGTH: 33
356 <212> TYPE: DNA
358 <213> ORGANISM: A1.3Bam
362 <400> SEQUENCE: 23
363 atatggatcc ctaagacatt tccatttcaa atg 33
366 <210> SEQ ID NO: 24
368 <211> LENGTH: 29
370 <212> TYPE: DNA
372 <213> ORGANISM: A2.5Nde
376 <400> SEQUENCE: 24
377 atatcatatg gatgttggtg ttgtgtgtg 29
380 <210> SEQ ID NO: 25
382 <211> LENGTH: 32
384 <212> TYPE: DNA
386 <213> ORGANISM: A2.3Bam
390 <400> SEQUENCE: 25
391 atatggatcc ctatgacatt tccatctgaa ag 32
394 <210> SEQ ID NO: 26
396 <211> LENGTH: 28
398 <212> TYPE: DNA
400 <213> ORGANISM: A1.I.Bam
404 <400> SEQUENCE: 26
405 cggatccccc acatttcaag tcgtgaat 28
408 <210> SEQ ID NO: 27
410 <211> LENGTH: 31
412 <212> TYPE: DNA
414 <213> ORGANISM: A1.I.Pst
418 <400> SEQUENCE: 27
419 gctgcagtca tattctttct cccagagttt t 31
422 <210> SEQ ID NO: 28
424 <211> LENGTH: 22
426 <212> TYPE: DNA
428 <213> ORGANISM: Primer specific for 5'EchPPK
432 <400> SEQUENCE: 28
433 gtagatgaca gtggcgtata tt 22
436 <210> SEQ ID NO: 29
438 <211> LENGTH: 23
440 <212> TYPE: DNA
442 <213> ORGANISM: Primer specific for 3'EchPPK
446 <400> SEQUENCE: 29
447 gccttaccat ttgtttaatt tgt 23
450 <210> SEQ ID NO: 30
452 <211> LENGTH: 159
454 <212> TYPE: PRT

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Input Set : A:\36470Asubseq.txt

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456 <213> ORGANISM: amino acid sequence of ???
460 <400> SEQUENCE: 30
462 Met Thr Val Ala Tyr Ile Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu
463 1 5 10 15
466 Glu Gln Val Asn Ala Ala Leu Lys Ala Leu Gly Asp Ile Pro Glu Ser
467 20 25 30
470 His Ile Leu Thr Val Ser Ser Phe Tyr Arg Thr Pro Pro Leu Gly Pro
471 35 40 45
474 Gln Asp Gln Pro Asp Tyr Leu Asn Ala Ala Val Ala Leu Glu Thr Ser
475 50 55 60
478 Leu Ala Pro Glu Glu Leu Asn His Thr Gln Arg Ile Glu Leu Gln
479 65 70 75 80
482 Gln Gly Arg Val Arg Lys Ala Glu Arg Trp Gly Pro Arg Thr Leu Asp
483 85 90 95
486 Leu Asp Ile Met Leu Phe Gly Asn Glu Val Ile Asn Thr Glu Arg Leu
487 100 105 110
490 Thr Val Pro His Tyr Asp Met Lys Asn Arg Gly Phe Met Leu Trp Pro
491 115 120 125
494 Leu Phe Glu Ile Ala Pro Glu Leu Val Phe Pro Asp Gly Glu Met Leu
495 130 135 140
498 Arg Gln Ile Leu His Thr Arg Ala Phe Asp Lys Leu Asn Lys Trp
499 145 150 155
502 <210> SEQ ID NO: 31
504 <211> LENGTH: 10
506 <212> TYPE: PRT
508 <213> ORGANISM: ???
512 <400> SEQUENCE: 31
514 Met Gly His His His His His Gly Gly
515 1 5 10
518 <210> SEQ ID NO: 32
520 <211> LENGTH: 52
522 <212> TYPE: DNA
524 <213> ORGANISM: 5'EcHisHPPK
528 <400> SEQUENCE: 32
529 cgccatgggc caccaccacc accaccacgg cggcatgaca gtggcgata tt 52
532 <210> SEQ ID NO: 33
534 <211> LENGTH: 29
536 <212> TYPE: DNA
538 <213> ORGANISM: 3'EcXhoHPPK
542 <400> SEQUENCE: 33
543 cggetcgagt taccatttgt ttaatttgt 29
546 <210> SEQ ID NO: 34
548 <211> LENGTH: 169
550 <212> TYPE: PRT
552 <213> ORGANISM: amino acid sequence of His(6)-HPPK gene
556 <400> SEQUENCE: 34
558 Met Gly His His His His His His Gly Gly Met Thr Val Ala Tyr Ile
559 1 5 10 15
562 Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu Glu Gln Val Asn Ala Ala

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**VERIFICATION SUMMARY**

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